Abstract P3-S7.16 Table 1 Association between *Lactobacillus* colonisation in the vagina and acquisition of bacterial vaginosis (BV)

Lactobacillus spp.	# BV acquisitions per woman-years	Rate Per 100 woman-years	Unadjusted HR (95% CI)	p Value
L crispatus				
Present	14/35.5	39	0.47 (0.24 to 0.90)	0.023
Absent	26/29.8	87		
L jensenii				
Present	18/22.6	80	1.42 (0.76 to 2.66)	0.270
Absent	22/42.7	52		
L gasseri				
Present	11/16.1	68	1.08 (0.54 to 2.17)	0.820
Absent	29/49.3	59		
L iners				
Present	13/20.2	64	1.13 (0.60 to 2.13)	0.695
Absent	27/45.1	60		

P3-S7.17 NONINVASIVE HIGH RESOLUTION IMAGING WITH OPTICAL COHERENCE TOMOGRAPHY FOR VAGINAL PRODUCT SAFETY ASSESSMENT IN WOMEN

doi:10.1136/sextrans-2011-050108.500

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Background Prevention of HIV and other STDs using vaginal microbicides must be safe. Colposcopy has not been shown to predict microbicide safety; therefore a more sensitive method is needed in safety evaluations of these vaginal products. The use of optical coherence tomography (OCT) has shown increased sensitivity to tissue injury over colposcopy in animal models. We describe a randomised double blind clinical trial using OCT to detect epithelial changes and injury related to vaginal microbicide use.
Methods 30 women aged 18–45 were randomised to use hydroxyethyl cellulose (HEC) placebo or nonoxynol-9 (N-9) vaginal gel twice daily for 5.5 days. Imaging with colposcopy and OCT was performed prior to product use, within 6 h of last dose of product, and 1 week after discontinuation of product. Colposcopy was graded based on vascular and epithelial disruption and erythema. OCT images were evaluated both by quantitative measurement of vaginal epithelial thickness and by use of a qualitative scoring system developed in the macaque to determine epithelial disruption and injury. Mixed model and significance of p=0.05 were used in data analysis.
Results Baseline colposcopy and OCT findings were similar between treatment groups. After treatment, there were no significant colposcopic differences in vascular or epithelial disruption between treatment groups, with only an increase in erythema noted after treatment in the N-9 group (p=0.01). OCT detected differences between groups in OCT scores (p<0.0001) and epithelial thickness, (p=0.008), both indicators of epithelial injury, after treatment with N-9. One week after discontinuation of treatment, OCT scores were similar between treatment groups (p=0.66) but epithelial thickness in the N-9 group was significantly thicker (p=0.0003).
Conclusions OCT can be used in a clinical setting to detect epithelial injury and is more sensitive than colposcopy to detect microscopic epithelial disruption. In addition, it gives information about the thickness of the epithelium, a measure previously available only through invasive biopsy. Vaginal epithelium thinned after treatment in the N-9 group, but then thickened after discontinuation of N-9, possibly due to post injury epithelial proliferation. OCT should be considered for inclusion in clinical trials for the detection of product-related toxicity to the vaginal and cervical epithelium.

P3-S7.18 AETIOLOGICAL AGENTS OF INFECTIVE VAGINAL DISCHARGE AMONG WOMEN ATTENDING A STD CLINIC IN KUMASI, GHANA

doi:10.1136/sextrans-2011-050108.501

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Objective To determine the prevalence of aetiological agents in Infective Vaginal Discharge among women attending a sexually transmitted infection (STI) clinic in Kumasi, Ghana. Methodology Three hundred (300) women consisting of 150 sex workers (SW) and 150 non-sex workers (NSW), attending the Suntreso STI clinic in Kumasi, with complaint of vaginal discharge were recruited for the study. Specimens for wet mount, pH determination, whiff test, Gram's stains, culture and polymerase chain reaction (PCR) were collected from the vagina and the cervix for microbial identification. The HIV status of the women was also determined by Western Blot Assay. Details regarding socio demographic characteristics of the women, symptoms and signs as well as sexual behaviour were recorded. Associations of these factors with each of the aetiological agent was recorded and adjusted for other risk factors.
Result Bacterial vaginosis was the most common cause of infective vaginal discharge (111/300: 37.0%, p =0.000, SW-61/150{40.7%}; NSW–58/150{38.0%} in the women, followed by *Candida spp.* (99/300: 32.7%, p=0.000, SW-41/150{27.3%}; NSW-58/150{38.0%}), *Trichomonas vaginalis* (20/300: 6.7%, p=0.000) SW-12/150{8.0%; NSW–8/150{5.3%}), *Chlamydia trachomatis* (9/300: 3.0%, p=0.001 SW–6/150{4.0%}; NSW-3/150{150{2.0%}), *Neisseria gonorrhoeae* (6/300: 2.0%, p=0.014, SW–4/150{2.7%}; NSW–2/150{1.3%}) and *Mycoplasma genitalium* (10/300, 3.3%, p=0.000, SW-7/150{2.0%}). 11.3% (34/300, 30 sex workers, four non-sex workers) of the women were HIV antibody positive. All of the aetiological agents except *Chlamydia trachomatis* (p=0.705) were associated with HIV infection. There was no difference in the types of aetiological agent found in sex workers (SW) and non-sex workers (NSW). Prevalence of all the aetiological agents was higher among sex workers except for *Candida spp.* (27.3%, 41/150 compared with non-sex workers (38.0%, 57/150). Younger age (15–29 years) was found to be the strongest predictor of infection.
Conclusion Agents of Bacteria vaginosis, *Candida spp.* and *Trachomonas vaginalis* continue to be the most predominant aetiological agents responsible for infective vaginal discharge among women in Kumasi, Ghana, while prevalence of *Neisseria gonorrhoeae* and *Chlamydia trachomatis* decline. Improving the detection and management of these organisms has significant public health implication for STI and possibly HIV control.

P3-S7.19 DIVERSITY OF THE VAGINAL FLORA DETERMINED BY MOLECULAR METHODS IN HEALTHY WOMEN AND WOMEN WITH BACTERIAL VAGINOSIS IN THE BAY AREA, CALIFORNIA, USA

doi:10.1136/sextrans-2011-050108.502

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Background The normal vaginal flora is primarily composed of *Lactobacillus spp.*, which maintain the vaginal pH and create an inhospitable environment for other organisms. Bacterial vaginosis

(BV) is a polymicrobial condition with low *Lactobacillus spp.* count and an increase in organisms such as *Mycoplasma hominis* and *Garderella vaginalis*. BV is associated with increased risk of acquisition of STDs/HIV and pregnancy-related morbidities. In this study, we described the general vaginal flora as well as the Lactobacillus spp of 10 healthy women and 10 women with BV in the Bay Area, California, USA.

Methods Between July 2009 and April 2010, we obtained vaginal swabs from 10 healthy women and 10 women with BV at the San Francisco City Clinic with informed consent. BV status was determined by Nugent scoring. The swabs were cultured in anaerobic conditions on Columbia agar, for unspecific bacterial growth, and on Rogosa agar, selective for *Lactobacillus spp*. By sequencing PCR amplifications of the 16srRNA gene, 5 to 10 single bacterial colonies from both agars were identified at the species level in all samples.

Abstract P3-S7.19 Table 1 Species Table US Data

		No. (%) of isolates in US collection	
Genus	**Species**	**BV−**	**BV+**
Actinomyces	*neuii*	0	1 (0.7)
Brevibacterium	*casei*	0	1 (0.7)
	ravenspurgense	1 (0.7)	0
Chryseobacterium	ND	0	1 (0.7)
Citrobacter	*koseri*	3 (2.1)	1 (0.7)
	ND	1 (0.7)	0
Corynebacterium	*amycolatum*	6 (4.2)	8 (6)
	aurimucosum	1 (0.7)	8 (6)
	coyleae	2 (1.4)	3 (2.2)
	simulans	0	1 (0.7)
	tuscaniae	0	2 (1.4)
	ND	2 (1.4)	3 (2.2)
Delftia	ND	0	1 (0.7)
Enterococcus	*faecalis*	15 (10.5)	10 (7.5)
Erwinia	ND	0	1 (0.7)
Escherichia	*coli*	0	5 (3.7)
Facklamia	*hominis*	0	1 (0.7)
Gardnerella	*vaginalis*	1 (0.7)	7 (5.2)
	ND	1 (0.7)	0
Gordonia	*polyisoprenivorans*	0	1 (0.7)
Lactobacillus	*coleohominis*	1 (0.7)	17 (12.7)
	crispatus	42 (29.4)	1 (0.7)
	gasseri	0	2 (1.5)
	iners	2 (1.4)	0
	jensenii	11 (7.7)	3 (2.2)
	johnsonii	4 (2.8)	3 (2.2)
	rhamnosus	3 (2.1)	0
	ruminis	0	2 (1.5)
	vaginalis	5 (3.5)	0
Microbacterium	ND	0	2 (1.5)
Proteus	*mirabilis*	1 (0.7)	0
Staphylococcus	*aureus*	0	1 (0.7)
	condimenti	1 (0.7)	0
	epidermidis	15 (10.5)	7 (5.2)
	haemolyticus	4 (2.8)	5 (3.7)
	hominis	4 (2.8)	1 (0.7)
	lugdunensis	2 (1.4)	2 (1.5)
	pasteuri	1 (0.7)	0
	simulans	0	1 (0.7)
	ND	1 (0.7)	5 (3.7)
Streptococcus	*agalactiae*	3 (2.1)	1 (0.7)
	anginosus	3 (2.1)	9 (6.7)
	cristatus	1 (0.7)	0
	mitis	2 (1.4)	1 (0.7)
	oralis	0	1 (0.7)
	pasteurianus	0	1 (0.7)
	salivarius	0	1 (0.7)
	ND	0	1 (0.7)
Tsukamurella	*tyrosinosolvens*	0	1 (0.7)
Total		143 (100)	134 (100)

Results A total of 277 bacterial colonies were successfully sequenced from healthy women (143) and women with BV (134). A wide range of organisms were identified in both groups. Corynebacterium spp were found in healthy women (11, 7.7%) and women with BV (25, 18.5%). Enterococcus faecalis was present in both groups (BV−: 15, 10.5%; BV+: 10, 7.5%). *Streptococcus spp* were found as well (BV−: 9, 6.3%; BV+: 15, 11.6%). *Staphylococcus spp.* were isolated (BV−: 28, 19.6%; BV+: 22, 16.2%), with *S epidermis* being the most common (BV−: 15, 10.5%; BV+: 7, 5.2%). Interestingly, *Gardnerella vaginalis* was isolated in one healthy woman in addition to women with BV (7, 5.2%). *Lactobacillus spp.* were found with higher frequency in healthy women (BV−: 68, 46.2%; BV+: 28, 20.8%). The most common species in healthy women were: *L crispatus* (42, 62% of total *Lactobacillus spp.*) and *L jensenii* (11, 16.2%). In women with BV, the most common was *L coleohominis* (17, 61%) see Abstract P3-S7.19 table 1.

Conclusions This pilot study with a sample size of 20 women gave important information regarding the diversity of the vaginal flora in healthy women and women with BV. There is a clear switch in *Lactobacillus spp.* dominance in health women vs women with BV. This finding sheds light on the association of specific *Lactobacillus spp.* with bacterial vaginosis.

Basic sciences poster session 1: *Chlamydia trachomatis* and *Neisseria gonorrehea*

P4-S1.01 ROLE OF *CHLAMYDIA TRACHOMATIS* HEAT SHOCK PROTEINS 60 AND 10 IN INDUCTION OF APOPTOSIS IN ENDOCERVICAL EPITHELIAL CELLS

doi:10.1136/sextrans-2011-050108.503

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Background Chlamydiae are known to modulate host cell to escape from immune response and prolong their persistence to cause fallopian tube damage, ectopic pregnancy and infertility. In addition, Chlamydiae have been reported to elicit both the induction of host cell death, or apoptosis, under some circumstances and actively inhibit apoptosis under others. Chlamydial heat shock proteins (cHSPs) have been known to be responsible for proinflammatory pathologic manifestations of human chlamydial disease in the reproductive tract. Moreover, cHSP60 has been shown to induce apoptosis, in vitro, in primary human trophoblasts, placental fibroblasts, and the JEG3 trophoblast cell line. However, no study has been dedicated to their potential role in apoptosis of primary cervical epithelial cells that are privilege target for chlamydial infection. In the present study, we investigated the ability of cHSP60 and cHSP10 to induce apoptosis in primary cervical epithelial cells.

Methods Primary cervical epithelial cells were stimulated with cHSP60 and cHSP10 for 4 h. Quantitative measurements of apoptosis have been performed by cytofluorometry and apoptosis-related genes were analysed by microarray, real-time PCR and western blotting. Further, levels ofd proinflammatory cytokines (IL-18 and IL-1ß) were determined by semi-quantitative RT-PCR.

Results Treatment with cHSP60 significantly increased the mean percentage of apoptotic cells (57.4±5.9 % vs 9.3±1.2 % in control cells, $p < 0.05$). Similarly, treatment with cHSP10 significantly